ABSTRACT OF THE DISCLOSURE

A bioinformatic method is provided for identifying and isolating proteins with MSCRAMM®-like characteristics from Gram positive bacteria, such as *Enterococcus, Staphylococcus, Streptococcus* and *Bacillus* bacteria, which can then be utilized in methods to prevent and treat infections caused by Gram-positive bacteria. The method involves identifying from sequence information those proteins with a putative C-terminal LPXTG (SEQ ID NO:1) cell wall sorting signal and other structural similarities to MSCRAMM® proteins having the LPXTG-anchored cell wall proteins. The MSCRAMM® proteins and immunogenic regions therein that are identified and isolated using the present invention may be used to generate antibodies useful in the diagnosis, treatment or prevention of Gram positive bacterial infections.